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SEQUENCE LISTING

<110> Adra, Chaker
<120> GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS AND USES THEREOF

<130> A0852.70000W000

<140> Not yet assigned
<141> 2005-03-03

<150> 60/549,865

<151> 2004-03-03

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<170> PatentIn version 3.3

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Lys Trp Arg Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr	
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Trp Phe Leu Phe Gly Val Ile Tyr Tyr Ala Ile Ala Phe Ile His Gly	
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Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr Trp Phe Leu
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Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His Ala Ile Phe
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Thr Cys Val Asp Ile Arg Trp Arg Trp Met Leu Val Ile Phe Cys Leu	
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Gly Gln Arg Tyr Leu Ala Asp Ile Phe Thr Thr Cys Val Asp Ile Arg			
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Gly Ile Asp Arg Ile Phe Leu Val Ser Pro Ile Thr Ile Val His Glu
260 265 270

Ile Asp Glu Asp Ser Pro Leu Tyr Asp Leu Ser Lys Gln Asp Ile Asp
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Thr Ala Met Thr Thr Gln Cys Arg Ser Ser Tyr Leu Ala Asn Glu Ile
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Leu Trp Gly His Arg Tyr Glu Pro Val Leu Phe Glu Glu Lys His Tyr

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325

330

335

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cag tgg ccc ggg acg tgg tgc ttc atc agc acc ggg cga ggg ggc aac Gln Trp Pro Gly Thr Trp Cys Phe Ile Ser Thr Gly Arg Gly Gly Asn	205	210	858
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ggg act agc tct tcg cat aac tgg ggc aac ctt ttc ttc gcc tct gcc Gly Thr Ser Ser His Asn Trp Gly Asn Leu Phe Phe Ala Ser Ala	220	225	906
			230
ttt gcc ttc ctg ggg ctc ttg gcg ctg aca gtc acc ttt tcc tgc aac Phe Ala Phe Leu Gly Leu Ala Leu Thr Val Thr Phe Ser Cys Asn	235	240	954
			245
ctg gcc acc att aag gcc ctg gtg tcc cgc tgc cg ^g gcc aag gcc acg Leu Ala Thr Ile Lys Ala Leu Val Ser Arg Cys Arg Ala Lys Ala Thr	250	255	1002
			260
			265
gca tct cag tcc agt gcc cag tgg ggc cgc atc acg acc gag acg gcc Ala Ser Gln Ser Ser Ala Gln Trp Gly Arg Ile Thr Thr Glu Thr Ala	270	275	1050
			280
att cag ctt atg ggg atc atg tgc gtg ctg tcg gtc tgg tct ccg Ile Gln Leu Met Gly Ile Met Cys Val Leu Ser Val Cys Trp Ser Pro	285	290	1098
			295
ctc ctg ata atg atg ttg aaa atg atc ttc aat cag aca tca gtt gag Leu Leu Ile Met Met Leu Lys Met Ile Phe Asn Gln Thr Ser Val Glu	300	305	1146
			310

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cac tgc aag aca cac acg gag aag cag aaa gaa tgc aac ttc ttc tta	1194
His Cys Lys Thr His Thr Glu Lys Gln Lys Glu Cys Asn Phe Phe Leu	
315 320 325	
ata gct gtt cgc ctg gct tca ctg aac cag atc ttg gat cct tgg gtt	1242
Ile Ala Val Arg Leu Ala Ser Leu Asn Gln Ile Leu Asp Pro Trp Val	
330 335 340 345	
tac ctg ctg tta aga aag atc ctt ctt cga aag ttt tgc cag atc agg	1290
Tyr Leu Leu Leu Arg Lys Ile Leu Leu Arg Lys Phe Cys Gln Ile Arg	
350 355 360	
tac cac aca aac aac tat gca tcc agc tcc acc tcc tta ccc tgc cag	1338
Tyr His Thr Asn Asn Tyr Ala Ser Ser Ser Thr Ser Leu Pro Cys Gln	
365 370 375	
tgt tcc tca acc ttg atg tgg agc gac cat ttg gaa aga taa	1380
Cys Ser Ser Thr Leu Met Trp Ser Asp His Leu Glu Arg	
380 385 390	
tgaaagaacg gagttggaca ttttattgca attcctgctt ccctgaattt gcataattct	1440
tcccacctga gaaggataat tatatatattt aatttggatt atttcttcat ttttatctt	1500
ttatTTtaat gattgttttgc ttagtaatac ccatggagat caactttattt attataatcc	1560
atgcctctga atattagagg gtttcttggaa tgggattttg aatatgcatt taagaacgtt	1620
gggaacaatt tcacagatga tgattggagg aaaagtgtatg aaaagaaaaga cctgtgttcc	1680
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gaaaagtcaa catattgaga gtgataattc aattaatagg atatgaactt aacgacat	1860
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atatttgc ccaattataa ccaatgtttt agagatgttgc tgcctctgtg gcttagcatg	1980
gaactaaaag ttcttaagtct caattcttagt tatgtgtcat ttagtaactc aggaatctgc	2040
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atccaggtag gccttctgtat tcaccatgac caagtcagga tttcttaata tttctttct	2220
ggcagcatat acaaaggcaa aattaataaa taacagttgt tgaataacaa actttattac	2280
gtttttataa aataaaagaa tctatTTgt ctgtattaaa ataaaaagct ttgtggactt	2340
ctaa	2344

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<212> PRT

<213> Homo sapiens

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- 14 -

Met Lys Glu Thr Arg Gly Tyr Gly Gly Asp Ala Pro Phe Cys Thr Arg
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Leu Asn His Ser Tyr Thr Gly Met Trp Ala Pro Glu Arg Ser Ala Glu
20 25 30

Ala Arg Gly Asn Leu Thr Arg Pro Pro Gly Ser Gly Glu Asp Cys Gly
35 40 45

Ser Val Ser Val Ala Phe Pro Ile Thr Met Leu Leu Thr Gly Phe Val
50 55 60

Gly Asn Ala Leu Ala Met Leu Leu Val Ser Arg Ser Tyr Arg Arg Arg
65 70 75 80

Glu Ser Lys Arg Lys Lys Ser Phe Leu Leu Cys Ile Gly Trp Leu Ala
85 90 95

Leu Thr Asp Leu Val Gly Gln Leu Leu Thr Thr Pro Val Val Ile Val
100 105 110

Val Tyr Leu Ser Lys Gln Arg Trp Glu His Ile Asp Pro Ser Gly Arg
115 120 125

Leu Cys Thr Phe Phe Gly Leu Thr Met Thr Val Phe Gly Leu Ser Ser
130 135 140

Leu Phe Ile Ala Ser Ala Met Ala Val Glu Arg Ala Leu Ala Ile Arg
145 150 155 160

Ala Pro His Trp Tyr Ala Ser His Met Lys Thr Arg Ala Thr Arg Ala
165 170 175

Val Leu Leu Gly Val Trp Leu Ala Val Leu Ala Phe Ala Leu Leu Pro
180 185 190

Val Leu Gly Val Gly Gln Tyr Thr Val Gln Trp Pro Gly Thr Trp Cys
195 200 205

Phe Ile Ser Thr Gly Arg Gly Asn Gly Thr Ser Ser Ser His Asn
210 215 220

Trp Gly Asn Leu Phe Phe Ala Ser Ala Phe Ala Phe Leu Gly Leu Leu
225 230 235 240

Ala Leu Thr Val Thr Phe Ser Cys Asn Leu Ala Thr Ile Lys Ala Leu
245 250 255

- 15 -

Val Ser Arg Cys Arg Ala Lys Ala Thr Ala Ser Gln Ser Ser Ala Gln
260 265 270

Trp Gly Arg Ile Thr Thr Glu Thr Ala Ile Gln Leu Met Gly Ile Met
275 280 285

Cys Val Leu Ser Val Cys Trp Ser Pro Leu Leu Ile Met Met Leu Lys
290 295 300

Met Ile Phe Asn Gln Thr Ser Val Glu His Cys Lys Thr His Thr Glu
305 310 315 320

Lys Gln Lys Glu Cys Asn Phe Phe Leu Ile Ala Val Arg Leu Ala Ser
325 330 335

Leu Asn Gln Ile Leu Asp Pro Trp Val Tyr Leu Leu Leu Arg Lys Ile
340 345 350

Leu Leu Arg Lys Phe Cys Gln Ile Arg Tyr His Thr Asn Asn Tyr Ala
355 360 365

Ser Ser Ser Thr Ser Leu Pro Cys Gln Cys Ser Ser Thr Leu Met Trp
370 375 380

Ser Asp His Leu Glu Arg
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Met Arg Gly Phe Asn Leu
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ctc ctc ttc tgg gga tgt tgt atg cac agc tgg gaa ggg cac ata
Leu Leu Phe Trp Gly Cys Cys Val Met His Ser Trp Glu Gly His Ile
10 15 20 104

aga ccc aca cgg aaa cca aac aca aag ggt aat aac tgt aga gac agt
Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly Asn Asn Cys Arg Asp Ser
25 30 35 152

acc ttg tgc cca gct tat gcc acc tgc acc aat aca gtg gac agt tac
200

- 16 -

Thr	Leu	Cys	Pro	Ala	Tyr	Ala	Thr	Cys	Thr	Asn	Thr	Val	Asp	Ser	Tyr	
40					45				50							
tat tgc gct tgc aaa caa ggc ttc ctg tcc agc aat ggg caa aat cac															248	
Tyr	Cys	Ala	Cys	Lys	Gln	Gly	Phe	Leu	Ser	Ser	Asn	Gly	Gln	Asn	His	
55					60				65						70	
ttc aag gat cca gga gtg cga tgc aaa gat att gat gaa tgt tct caa															296	
Phe	Lys	Asp	Pro	Gly	Val	Arg	Cys	Lys	Asp	Ile	Asp	Glu	Cys	Ser	Gln	
					75				80						85	
agc ccc cag ccc tgt ggt cct aac tca tcc tgc aaa aac ctg tca ggg															344	
Ser	Pro	Gln	Pro	Cys	Gly	Pro	Asn	Ser	Ser	Cys	Lys	Asn	Leu	Ser	Gly	
					90				95						100	
agg tac aag tgc agc tgt tta gat ggt ttc tct tct ccc act gga aat															392	
Arg	Tyr	Lys	Cys	Ser	Cys	Leu	Asp	Gly	Phe	Ser	Ser	Pro	Thr	Gly	Asn	
					105				110						115	
gac tgg gtc cca gga aag ccg ggc aat ttc tcc tgt act gat atc aat															440	
Asp	Trp	Val	Pro	Gly	Lys	Pro	Gly	Asn	Phe	Ser	Cys	Thr	Asp	Ile	Asn	
					120				125						130	
gag tgc ctc acc agc agc gtc tgc cct gag cat tct gac tgt gtc aac															488	
Glu	Cys	Leu	Thr	Ser	Ser	Val	Cys	Pro	Glu	His	Ser	Asp	Cys	Val	Asn	
					135				140						150	
tcc atg gga agc tac agt tgc agc tgt caa gtt gga ttc atc tct aga															536	
Ser	Met	Gly	Ser	Tyr	Ser	Cys	Ser	Cys	Gln	Val	Gly	Phe	Ile	Ser	Arg	
					155				160						165	
aac tcc acc tgt gaa gac gtg gat gaa tgt gca gat cca aga gct tgc															584	
Asn	Ser	Thr	Cys	Glu	Asp	Val	Asp	Glu	Cys	Ala	Asp	Pro	Arg	Ala	Cys	
					170				175						180	
cca gag cat gca act tgt aat aac act gtt gga aac tac tct tgt ttc															632	
Pro	Glu	His	Ala	Thr	Cys	Asn	Asn	Thr	Val	Gly	Asn	Tyr	Ser	Cys	Phe	
					185				190						195	
tgc aac cca gga ttt gaa tcc agc agt ggc cac ttg agt ttc cag ggt															680	
Cys	Asn	Pro	Gly	Phe	Glu	Ser	Ser	Gly	His	Leu	Ser	Phe	Gln	Gly		
					200				205						210	
ctc aaa gca tcg tgt gaa gat att gat gaa tgc act gaa atg tgc ccc															728	
Leu	Lys	Ala	Ser	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Thr	Glu	Met	Cys	Pro	
					215				220						230	
atc aat tca aca tgc acc aac act cct ggg agc tac ttt tgc acc tgc															776	
Ile	Asn	Ser	Thr	Cys	Thr	Asn	Thr	Pro	Gly	Ser	Tyr	Phe	Cys	Thr	Cys	
					235				240						245	
cac cct ggc ttt gca cca agc aat gga cag ttg aat ttc aca gac caa															824	
His	Pro	Gly	Phe	Ala	Pro	Ser	Asn	Gly	Gln	Leu	Asn	Phe	Thr	Asp	Gln	
					250				255						260	
gga gtg gaa tgt aga gat att gat gag tgc cgc caa gat cca tca acc															872	
Gly	Val	Glu	Cys	Arg	Asp	Ile	Asp	Glu	Cys	Arg	Gln	Asp	Pro	Ser	Thr	
					265				270						275	
tgt ggt cct aat tct atc tgc acc aat gcc ctg ggc tcc tac agc tgt															920	
Cys	Gly	Pro	Asn	Ser	Ile	Cys	Thr	Asn	Ala	Leu	Gly	Ser	Tyr	Ser	Cys	
					280				285						290	

ggc tgc att gca ggc ttt cat ccc aat cca gaa ggc tcc cag aaa gat	968
Gly Cys Ile Ala Gly Phe His Pro Asn Pro Glu Gly Ser Gln Lys Asp	
295 300 305 310	
ggc aac ttc agc tgc caa agg gtt ctc ttc aaa tgt aag gaa gat gtg	1016
Gly Asn Phe Ser Cys Gln Arg Val Leu Phe Lys Cys Lys Glu Asp Val	
315 320 325	
ata ccc gat aat aag cag atc cag caa tgc caa gag gga acc gca gtg	1064
Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys Gln Glu Gly Thr Ala Val	
330 335 340	
aaa cct gca tat gtc tcc ttt tgt gca caa ata aat aac atc ttc agc	1112
Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln Ile Asn Asn Ile Phe Ser	
345 350 355	
gtt ctg gac aaa gtg tgt gaa aat aaa acg acc gta gtt tct ctg aag	1160
Val Leu Asp Lys Val Cys Glu Asn Lys Thr Thr Val Val Ser Leu Lys	
360 365 370	
aat aca act gag agc ttt gtc cct gtg ctt aaa caa ata tcc acg tgg	1208
Asn Thr Thr Glu Ser Phe Val Pro Val Leu Lys Gln Ile Ser Thr Trp	
375 380 385 390	
act aaa ttc acc aag gaa gag acg tcc tcc ctg gcc aca gtc ttc ctg	1256
Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser Leu Ala Thr Val Phe Leu	
395 400 405	
gag agt gtg gaa agc atg aca ctg gca tct ttt tgg aaa ccc tca gca	1304
Glu Ser Val Glu Ser Met Thr Leu Ala Ser Phe Trp Lys Pro Ser Ala	
410 415 420	
aat atc act ccg gct gtt cgg acg gaa tac tta gac att gag agc aaa	1352
Asn Ile Thr Pro Ala Val Arg Thr Glu Tyr Leu Asp Ile Glu Ser Lys	
425 430 435	
gtt atc aac aaa gaa tgc agt gaa gag aat gtg acg ttg gac ttg gta	1400
Val Ile Asn Lys Glu Cys Ser Glu Glu Asn Val Thr Leu Asp Leu Val	
440 445 450	
gcc aag ggg gat aag atg aag atc ggg tgt tcc aca att gag gaa tct	1448
Ala Lys Gly Asp Lys Met Lys Ile Gly Cys Ser Thr Ile Glu Glu Ser	
455 460 465 470	
gaa tcc aca gag acc act ggt gtg gct ttt gtc tcc ttt gtg ggc atg	1496
Glu Ser Thr Glu Thr Gly Val Ala Phe Val Ser Phe Val Gly Met	
475 480 485	
gaa tcg gtt tta aat gag cgc ttc ttc aaa gac cac cag gct ccc ttg	1544
Glu Ser Val Leu Asn Glu Arg Phe Phe Lys Asp His Gln Ala Pro Leu	
490 495 500	
acc acc tct gag atc aag ctg aag atg aat tct cga gtc gtt ggg ggc	1592
Thr Thr Ser Glu Ile Lys Leu Lys Met Asn Ser Arg Val Val Gly Gly	
505 510 515	
ata atg act gga gag aag aaa gac ggc ttc tca gat cca atc atc tac	1640
Ile Met Thr Gly Glu Lys Lys Asp Gly Phe Ser Asp Pro Ile Ile Tyr	
520 525 530	
act ctg gag aac att cag cca aag cag aag ttt gag agg ccc atc tgt	1688

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Thr	Leu	Glu	Asn	Ile	Gln	Pro	Lys	Gln	Lys	Phe	Glu	Arg	Pro	Ile	Cys	
535					540				545					550		
gtt	tcc	tgg	agc	act	gat	gtg	aag	ggt	gga	aga	tgg	aca	tcc	ttt	ggc	1736
Val	Ser	Trp	Ser	Thr	Asp	Val	Lys	Gly	Gly	Arg	Trp	Thr	Ser	Phe	Gly	
					555				560				565			
tgt	gtg	atc	ctg	gaa	gct	tct	gag	aca	tat	acc	atc	tgc	agc	tgt	aat	1784
Cys	Val	Ile	Leu	Glu	Ala	Ser	Glu	Thr	Tyr	Thr	Ile	Cys	Ser	Cys	Asn	
					570				575			580				
cag	atg	gca	aat	ctt	gcc	gtt	atc	atg	gcg	tct	ggg	gag	ctc	acg	atg	1832
Gln	Met	Ala	Asn	Leu	Ala	Val	Ile	Met	Ala	Ser	Gly	Glu	Leu	Thr	Met	
					585				590			595				
gac	ttt	tcc	ttg	tac	atc	att	agc	cat	gta	ggc	att	atc	atc	tcc	ttg	1880
Asp	Phe	Ser	Leu	Tyr	Ile	Ile	Ser	His	Val	Gly	Ile	Ile	Ile	Ser	Leu	
					600				605			610				
gtg	tgc	ctc	gtc	ttg	gcc	atc	gcc	acc	ttt	ctg	ctg	tgt	cgc	tcc	atc	1928
Val	Cys	Leu	Val	Leu	Ala	Ile	Ala	Thr	Phe	Leu	Leu	Cys	Arg	Ser	Ile	
					615				620			625		630		
cga	aat	cac	aac	acc	tac	ctc	cac	ctg	cac	ctc	tgc	gtg	tgt	ctc	ctc	1976
Arg	Asn	His	Asn	Thr	Tyr	Leu	His	Leu	His	Leu	Cys	Val	Cys	Leu	Leu	
					635				640			645				
ttg	gcg	aag	act	ctc	tcc	ctc	gcc	ggt	ata	cac	aag	act	gac	aac	aag	2024
Leu	Ala	Lys	Thr	Leu	Phe	Leu	Ala	Gly	Ile	His	Lys	Thr	Asp	Asn	Lys	
					650				655			660				
atg	ggc	tgc	gcc	atc	atc	gcg	ggc	ttc	ctg	cac	tac	ctt	ttc	ttt	gcc	2072
Met	Gly	Cys	Ala	Ile	Ile	Ala	Gly	Phe	Leu	His	Tyr	Leu	Phe	Leu	Ala	
					665				670			675				
tgc	tcc	ttc	tgg	atg	ctg	gtg	gag	gct	gtg	ata	ctg	ttc	ttg	atg	gtc	2120
Cys	Phe	Phe	Trp	Met	Leu	Val	Glu	Ala	Val	Ile	Leu	Phe	Leu	Met	Val	
					680				685			690				
aga	aac	ctg	aag	gtg	gtg	aat	tac	tcc	agc	tct	cgc	aac	atc	aag	atg	2168
Arg	Asn	Leu	Lys	Val	Val	Asn	Tyr	Phe	Ser	Ser	Arg	Asn	Ile	Lys	Met	
					695				700			705		710		
ctg	cac	atc	tgt	gcc	ttt	ggt	tat	ggg	ctg	ccg	atg	ctg	gtg	gtg	gtg	2216
Leu	His	Ile	Cys	Ala	Phe	Gly	Tyr	Gly	Leu	Pro	Met	Leu	Val	Val	Val	
					715				720			725				
atc	tct	gcc	agt	gtg	cag	cca	cag	ggc	tat	gga	atg	cat	aat	cgc	tgc	2264
Ile	Ser	Ala	Ser	Val	Gln	Pro	Gln	Gly	Tyr	Gly	Met	His	Asn	Arg	Cys	
					730				735			740				
tgg	ctg	aat	aca	gag	aca	ggg	ttc	atc	tgg	agt	ttc	ttg	ggg	cca	gtt	2312
Trp	Leu	Asn	Thr	Glu	Thr	Gly	Phe	Ile	Trp	Ser	Phe	Leu	Gly	Pro	Val	
					745				750			755				
tgc	aca	gtt	ata	gtg	atc	aac	tcc	ctt	ctc	ctg	acc	tgg	acc	ttg	tgg	2360
Cys	Thr	Val	Ile	Val	Ile	Asn	Ser	Leu	Leu	Leu	Thr	Trp	Thr	Leu	Trp	
					760				765			770				
atc	ctg	agg	cag	agg	ctt	tcc	agt	gtt	aat	gcc	gaa	gtc	tca	acg	cta	2408
Ile	Leu	Arg	Gln	Arg	Leu	Ser	Ser	Val	Asn	Ala	Glu	Val	Ser	Thr	Leu	
					775				780			785		790		

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aaa gac acc agg tta ctg acc ttc aag gcc ttt gcc cag ctc ttc atc	2456
Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala Phe Ala Gln Leu Phe Ile	
795 800 805	
ctg ggc tgc tcc tgg gtg ctg ggc att ttt cag att gga cct gtg gca	2504
Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly Pro Val Ala	
810 815 820	
ggt gtc atg gct tac ctg ttc acc atc atc aac agc ctg cag ggg gcc	2552
Gly Val Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu Gln Gly Ala	
825 830 835	
ttc atc ttc ctc atc cac tgt ctg ctc aac ggc cag gta cga gaa gaa	2600
Phe Ile Phe Leu Ile His Cys Leu Leu Asn Gly Gln Val Arg Glu Glu	
840 845 850	
tac aag agg tgg atc act ggg aag acg aag ccc agc tcc cag tcc cag	2648
Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys Pro Ser Ser Gln Ser Gln	
855 860 865 870	
acc tca agg atc ttg ctg tcc tcc atg cca tcc gct tcc aag acg ggt	2696
Thr Ser Arg Ile Leu Leu Ser Ser Met Pro Ser Ala Ser Lys Thr Gly	
875 880 885	
taa agtcctttct tgctttcaaa tatgctatgg agccacagtt gaggacagta	2749
gtttcctgca ggagcctacc ctgaaatctc ttctcagctt aacatggaaa tgaggatccc	2809
accagccccca gaaccctctg gggagaatg ttggggggcgg tcttcctgtg gttgtatgca	2869
ctgatgagaa atcaggcggt tctgctccaa acgaccattt tatcttcgtg ctctgcaact	2929
tcttcaattc cagagtttct gagaacagac ccaaattcaa tggcatgacc aagaacacct	2989
ggctaccatt ttgtttctc ctgcccattgt tggtgcattt ttcttaagcat gcccctccag	3049
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<400> 9

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Ser Trp Glu Gly His Ile Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly
 20 25 30

Asn Asn Cys Arg Asp Ser Thr Leu Cys Pro Ala Tyr Ala Thr Cys Thr
 35 40 45

Asn Thr Val Asp Ser Tyr Tyr Cys Ala Cys Lys Gln Gly Phe Leu Ser

- 20 -

50	55	60
Ser Asn Gly Gln Asn His Phe Lys Asp Pro Gly Val Arg Cys Lys Asp		
65	70	75
Ile Asp Glu Cys Ser Gln Ser Pro Gln Pro Cys Gly Pro Asn Ser Ser		
85	90	95
Cys Lys Asn Leu Ser Gly Arg Tyr Lys Cys Ser Cys Leu Asp Gly Phe		
100	105	110
Ser Ser Pro Thr Gly Asn Asp Trp Val Pro Gly Lys Pro Gly Asn Phe		
115	120	125
Ser Cys Thr Asp Ile Asn Glu Cys Leu Thr Ser Ser Val Cys Pro Glu		
130	135	140
His Ser Asp Cys Val Asn Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln		
145	150	155
160		
Val Gly Phe Ile Ser Arg Asn Ser Thr Cys Glu Asp Val Asp Glu Cys		
165	170	175
Ala Asp Pro Arg Ala Cys Pro Glu His Ala Thr Cys Asn Asn Thr Val		
180	185	190
Gly Asn Tyr Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly		
195	200	205
His Leu Ser Phe Gln Gly Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu		
210	215	220
Cys Thr Glu Met Cys Pro Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly		
225	230	240
Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Pro Ser Asn Gly Gln		
245	250	255
Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp Glu Cys		
260	265	270
Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala		
275	280	285
Leu Gly Ser Tyr Ser Cys Gly Cys Ile Ala Gly Phe His Pro Asn Pro		
290	295	300

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Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys Gln Arg Val Leu Phe
305 310 315 320

Lys Cys Lys Glu Asp Val Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys
325 330 335

Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln
340 345 350

Ile Asn Asn Ile Phe Ser Val Leu Asp Lys Val Cys Glu Asn Lys Thr
355 360 365

Thr Val Val Ser Leu Lys Asn Thr Thr Glu Ser Phe Val Pro Val Leu
370 375 380

Lys Gln Ile Ser Thr Trp Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser
385 390 395 400

Leu Ala Thr Val Phe Leu Glu Ser Val Glu Ser Met Thr Leu Ala Ser
405 410 415

Phe Trp Lys Pro Ser Ala Asn Ile Thr Pro Ala Val Arg Thr Glu Tyr
420 425 430

Leu Asp Ile Glu Ser Lys Val Ile Asn Lys Glu Cys Ser Glu Glu Asn
435 440 445

Val Thr Leu Asp Leu Val Ala Lys Gly Asp Lys Met Lys Ile Gly Cys
450 455 460

Ser Thr Ile Glu Glu Ser Glu Ser Thr Glu Thr Thr Gly Val Ala Phe
465 470 475 480

Val Ser Phe Val Gly Met Glu Ser Val Leu Asn Glu Arg Phe Phe Lys
485 490 495

Asp His Gln Ala Pro Leu Thr Thr Ser Glu Ile Lys Leu Lys Met Asn
500 505 510

Ser Arg Val Val Gly Gly Ile Met Thr Gly Glu Lys Lys Asp Gly Phe
515 520 525

Ser Asp Pro Ile Ile Tyr Thr Leu Glu Asn Ile Gln Pro Lys Gln Lys
530 535 540

Phe Glu Arg Pro Ile Cys Val Ser Trp Ser Thr Asp Val Lys Gly Gly

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545 550 555 560

Arg Trp Thr Ser Phe Gly Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr
565 570 575

Thr Ile Cys Ser Cys Asn Gln Met Ala Asn Leu Ala Val Ile Met Ala
580 585 590

Ser Gly Glu Leu Thr Met Asp Phe Ser Leu Tyr Ile Ile Ser His Val
595 600 605

Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe
610 615 620

Leu Leu Cys Arg Ser Ile Arg Asn His Asn Thr Tyr Leu His Leu His
625 630 635 640

Leu Cys Val Cys Leu Leu Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile
645 650 655

His Lys Thr Asp Asn Lys Met Gly Cys Ala Ile Ile Ala Gly Phe Leu
660 665 670

His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val
675 680 685

Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser
690 695 700

Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu
705 710 715 720

Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr
725 730 735

Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp
740 745 750

Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu
755 760 765

Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn
770 775 780

Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala
785 790 795 800

- 23 -

Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe
805 810 815

Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile
820 825 830

Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn
835 840 845

Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys
850 855 860

Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro
865 870 875 880

Ser Ala Ser Lys Thr Gly
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<213> Homo sapiens

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aaacgctcac tggcaaaac accttcactg aaaagagacc tcataattatg caaaaaaaaat 120
cttaaaaggc ctctgccttc agaagttaca ag atg atc aat tca acc tcc aca 180
Met Ile Asn Ser Thr Ser Thr
1 5
233

cag cct cca gat gaa tcc tgc tct cag aac ctc ctg atc act cag cag 281
Gln Pro Pro Asp Glu Ser Cys Ser Gln Asn Leu Leu Ile Thr Gln Gln
10 15 20

atc att cct gtg ctg tac tgt atg gtc ttc att gca gga atc cta ctc 329
Ile Ile Pro Val Leu Tyr Cys Met Val Phe Ile Ala Gly Ile Leu Leu
25 30 35

aat gga gtg tca gga tgg ata ttc ttt tac gtg ccc agc tct gag agt 377
Asn Gly Val Ser Gly Trp Ile Phe Phe Tyr Val Pro Ser Ser Glu Ser
40 45 50 55

ttc atc atc tat ctc aag aac att gtt att gct gac ttt gtg atg agc 425
Phe Ile Ile Tyr Leu Lys Asn Ile Val Ile Ala Asp Phe Val Met Ser
60 65 70

- 24 -

ctg act ttt cct ttc aag atc ctt ggt gac tca ggc ctt ggt ccc tgg	473
Leu Thr Phe Pro Phe Lys Ile Leu Gly Asp Ser Gly Leu Gly Pro Trp	
75 80 85	
cag ctg aac gtg ttt gtg tgc agg gtc tct gcc gtg ctc ttc tac gtc	521
Gln Leu Asn Val Phe Val Cys Arg Val Ser Ala Val Leu Phe Tyr Val	
90 95 100	
aac atg tac gtc agc att gtg ttc ttt ggg ctc atc agc ttt gac aga	569
Asn Met Tyr Val Ser Ile Val Phe Phe Gly Leu Ile Ser Phe Asp Arg	
105 110 115	
tat tat aaa att gta aag cct ctt tgg act tct ttc atc cag tca gtg	617
Tyr Tyr Lys Ile Val Lys Pro Leu Trp Thr Ser Phe Ile Gln Ser Val	
120 125 130 135	
agt tac agc aaa ctt ctg tca gtg ata gta tgg atg ctc atg ctc ctc	665
Ser Tyr Ser Lys Leu Leu Ser Val Ile Val Trp Met Leu Met Leu Leu	
140 145 150	
ctt gct gtt cca aat att att ctc acc aac cag agt gtt agg gag gtt	713
Leu Ala Val Pro Asn Ile Ile Leu Thr Asn Gln Ser Val Arg Glu Val	
155 160 165	
aca caa ata aaa tgt ata gaa ctg aaa agt gaa ctg gga cgg aag tgg	761
Thr Gln Ile Lys Cys Ile Glu Leu Lys Ser Glu Leu Gly Arg Lys Trp	
170 175 180	
cac aaa gca tca aac tac atc ttc gtg gcc atc ttc tgg att gtg ttt	809
His Lys Ala Ser Asn Tyr Ile Phe Val Ala Ile Phe Trp Ile Val Phe	
185 190 195	
ctt ttg tta atc gtt ttc tat act gct atc aca aag aaa atc ttt aag	857
Leu Leu Leu Ile Val Phe Tyr Thr Ala Ile Thr Lys Lys Ile Phe Lys	
200 205 210 215	
tcc cac ctt aag tca agt cgg aat tcc act tcg gtc aaa aag aaa tct	905
Ser His Leu Lys Ser Ser Arg Asn Ser Thr Ser Val Lys Lys Lys Ser	
220 225 230	
agc cgc aac ata ttc agc atc gtg ttt gtg ttt ttt gtc tgt ttt gta	953
Ser Arg Asn Ile Phe Ser Ile Val Phe Val Phe Phe Val Cys Phe Val	
235 240 245	
cct tac cat att gcc aga atc ccc tac aca aag agt cag acc gaa gct	1001
Pro Tyr His Ile Ala Arg Ile Pro Tyr Thr Lys Ser Gln Thr Glu Ala	
250 255 260	
cat tac agc tgc cag tca aaa gaa atc ttg cgg tat atg aaa gaa ttc	1049
His Tyr Ser Cys Gln Ser Lys Glu Ile Leu Arg Tyr Met Lys Glu Phe	
265 270 275	
act ctg cta cta tct gct gca aat gta tgc ttg gac cct att att tat	1097
Thr Leu Leu Leu Ser Ala Ala Asn Val Cys Leu Asp Pro Ile Ile Tyr	
280 285 290 295	
ttc ttt cta tgc cag ccg ttt agg gaa atc tta tgt aag aaa ttg cac	1145
Phe Phe Leu Cys Gln Pro Phe Arg Glu Ile Leu Cys Lys Lys Leu His	
300 305 310	
att cca tta aaa gct cag aat gac cta gac att tcc aga atc aaa aga	1193
Ile Pro Leu Lys Ala Gln Asn Asp Leu Asp Ile Ser Arg Ile Lys Arg	

- 25 -

315

320

325

gga aat aca aca ctt gaa agc aca gat act ttg tga gttcctaccc 1239
Gly Asn Thr Thr Leu Glu Ser Thr Asp Thr Leu
330 335

tcttccaaag aaagaccacg tgtgcattt gtcatcttca attacataac agaaatcaat 1299
aagatatgtg ccctcatcat aaatatcatc tctagcactg ccatccaatt tagttcaata 1359
aaattcaaat ataagttcc atgcttttt gtaacatcaa agaaaacata cccatcagta 1419
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caattctatt atattaaaat aagttaaagt ttataaccac tagtctggc agttaatgta 1539
gaaatttaaa tagtaaataa aacacaacat aatcaaagac aactcactca ggcattttct 1599
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tctaaaattt acattaatga gtgcaaaata acacataaaa tgaaaattca cacatcacat 2199
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agctaccaaa actaaattct ttctctgcta ttaactggct agaagacatt catctatttt 2319
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tctatataact aataaaqaaa tqtttaata ccqaaaaaaaaaaaaaaa 2428

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<212> PRT
<213> *Homo sapiens*

<400> 11

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Asn Leu Leu Ile Thr Gln Gln Ile Ile Pro Val Leu Tyr Cys Met Val
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- 26 -

Phe Ile Ala Gly Ile Leu Leu Asn Gly Val Ser Gly Trp Ile Phe Phe
35 40 45

Tyr Val Pro Ser Ser Glu Ser Phe Ile Ile Tyr Leu Lys Asn Ile Val
50 55 60

Ile Ala Asp Phe Val Met Ser Leu Thr Phe Pro Phe Lys Ile Leu Gly
65 70 75 80

Asp Ser Gly Leu Gly Pro Trp Gln Leu Asn Val Phe Val Cys Arg Val
85 90 95

Ser Ala Val Leu Phe Tyr Val Asn Met Tyr Val Ser Ile Val Phe Phe
100 105 110

Gly Leu Ile Ser Phe Asp Arg Tyr Tyr Lys Ile Val Lys Pro Leu Trp
115 120 125

Thr Ser Phe Ile Gln Ser Val Ser Tyr Ser Lys Leu Leu Ser Val Ile
130 135 140

Val Trp Met Leu Met Leu Leu Ala Val Pro Asn Ile Ile Leu Thr
145 150 155 160

Asn Gln Ser Val Arg Glu Val Thr Gln Ile Lys Cys Ile Glu Leu Lys
165 170 175

Ser Glu Leu Gly Arg Lys Trp His Lys Ala Ser Asn Tyr Ile Phe Val
180 185 190

Ala Ile Phe Trp Ile Val Phe Leu Leu Ile Val Phe Tyr Thr Ala
195 200 205

Ile Thr Lys Lys Ile Phe Lys Ser His Leu Lys Ser Ser Arg Asn Ser
210 215 220

Thr Ser Val Lys Lys Lys Ser Ser Arg Asn Ile Phe Ser Ile Val Phe
225 230 235 240

Val Phe Phe Val Cys Phe Val Pro Tyr His Ile Ala Arg Ile Pro Tyr
245 250 255

Thr Lys Ser Gln Thr Glu Ala His Tyr Ser Cys Gln Ser Lys Glu Ile
260 265 270

Leu Arg Tyr Met Lys Glu Phe Thr Leu Leu Leu Ser Ala Ala Asn Val
275 280 285

Cys Leu Asp Pro Ile Ile Tyr Phe Phe Leu Cys Gln Pro Phe Arg Glu
 290 295 300

Ile Leu Cys Lys Lys Leu His Ile Pro Leu Lys Ala Gln Asn Asp Leu
 305 310 315 320

Asp Ile Ser Arg Ile Lys Arg Gly Asn Thr Thr Leu Glu Ser Thr Asp
 325 330 335

Thr Leu

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<211> 1734

<212> DNA

<213> Homo sapiens

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tctgcggcgt gactggaggc ccag atg gtc atc atg ggc cag tgc tac tac 111
 Met Val Ile Met Gly Gln Cys Tyr Tyr
 1 5

aac gag acc atc ggc ttc ttc tat aac aac agt ggc aaa gag ctc agc 159
 Asn Glu Thr Ile Gly Phe Phe Tyr Asn Asn Ser Gly Lys Glu Leu Ser
 10 15 20 25

tcc cac tgg cgg ccc aag gat gtg gtc gtg gca ctg ggg ctg acc 207
 Ser His Trp Arg Pro Lys Asp Val Val Val Val Ala Leu Gly Leu Thr
 30 35 40

gtc agc gtg ctg gtg ctg acc aat ctg ctg gtc ata gca gcc atc 255
 Val Ser Val Leu Val Leu Leu Thr Asn Leu Leu Val Ile Ala Ala Ile
 45 50 55

gcc tcc aac cgc cgc ttc cac cag ccc atc tac tac ctg ctc ggc aat 303
 Ala Ser Asn Arg Arg Phe His Gln Pro Ile Tyr Tyr Leu Leu Gly Asn
 60 65 70

ctg gcc gcg gct gac ctc ttc gcg ggc gtg gcc tac ctc ttc ctc atg 351
 Leu Ala Ala Ala Asp Leu Phe Ala Gly Val Ala Tyr Leu Phe Leu Met
 75 80 85

ttc cac act ggt ccc cgc aca gcc cga ctt tca ctt gag ggc tgg ttc 399
 Phe His Thr Gly Pro Arg Thr Ala Arg Leu Ser Leu Glu Gly Trp Phe
 90 95 100 105

ctg cgg cag ggc ttg ctg gac aca agc ctc act gcg tcg gtg gcc aca 447
 Leu Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Val Ala Thr
 110 115 120

ctg ctg gcc atc gcc gtg gag cgg cac cgc agt gtg atg gcc gtg cag	495
Leu Leu Ala Ile Ala Val Glu Arg His Arg Ser Val Met Ala Val Gln	
125 130 135	
ctg cac agc cgc ctg ccc cgt ggc cgc gtg gtc atg ctc att gtg ggc	543
Leu His Ser Arg Leu Pro Arg Gly Arg Val Val Met Leu Ile Val Gly	
140 145 150	
gtg tgg gtg gct gcc ctg ggc ctg ggg ctg ctg cct gcc cac tcc tgg	591
Val Trp Val Ala Ala Leu Gly Leu Gly Leu Leu Pro Ala His Ser Trp	
155 160 165	
cac tgc ctc tgt gcc ctg gac cgc tgc tca cgc atg gca ccc ctg ctc	639
His Cys Leu Cys Ala Leu Asp Arg Cys Ser Arg Met Ala Pro Leu Leu	
170 175 180 185	
agc cgc tcc tat ttg gcc gtc tgg gct ctg tcg agc ctg ctt gtc ttc	687
Ser Arg Ser Tyr Leu Ala Val Trp Ala Leu Ser Ser Leu Leu Val Phe	
190 195 200	
ctg ctc atg gtg gct gtg tac acc cgc att ttc ttc tac gtg cgg cgg	735
Leu Leu Met Val Ala Val Tyr Thr Arg Ile Phe Phe Tyr Val Arg Arg	
205 210 215	
cga gtg cag cgc atg gca gag cat gtc agc tgc cac ccc cgc tac cga	783
Arg Val Gln Arg Met Ala Glu His Val Ser Cys His Pro Arg Tyr Arg	
220 225 230	
gag acc acg ctc agc ctg gtc aag act gtt gtc atc atc ctg ggg gcg	831
Glu Thr Thr Leu Ser Leu Val Lys Thr Val Val Ile Ile Leu Gly Ala	
235 240 245	
ttc gtg gtc tgc tgg aca cca ggc cag gtg gta ctg ctc ctg gat ggt	879
Phe Val Val Cys Trp Thr Pro Gly Gln Val Val Leu Leu Leu Asp Gly	
250 255 260 265	
tta ggc tgt gag tcc tgc aat gtc ctg gct gta gaa aag tac ttc cta	927
Leu Gly Cys Glu Ser Cys Asn Val Leu Ala Val Glu Lys Tyr Phe Leu	
270 275 280	
ctg ttg gcc gag gcc aac tca ctg gtc aat gct gct gtg tac tct tgc	975
Leu Leu Ala Glu Ala Asn Ser Leu Val Asn Ala Ala Val Tyr Ser Cys	
285 290 295	
cga gat gct gag atg cgc cgc acc ttc cgc cgc ctt ctc tgc tgc gcg	1023
Arg Asp Ala Glu Met Arg Arg Thr Phe Arg Arg Leu Leu Cys Cys Ala	
300 305 310	
tgc ctc cgc cag tcc acc cgc gag tct gtc cac tat aca tcc tct gcc	1071
Cys Leu Arg Gln Ser Thr Arg Glu Ser Val His Tyr Thr Ser Ser Ala	
315 320 325	
cag gga ggt gcc agc act cgc atc atg ctt ccc gag aac ggc cac cca	1119
Gln Gly Gly Ala Ser Thr Arg Ile Met Leu Pro Glu Asn Gly His Pro	
330 335 340 345	
ctg atg act cca ccc ttt agc tac ctt gaa ctt cag cgg tac gcg gca	1167
Leu Met Thr Pro Pro Phe Ser Tyr Leu Glu Leu Gln Arg Tyr Ala Ala	
350 355 360	
agc aac aaa tcc aca gcc cct gat gac ttg tgg gtg ctc ctg gct caa	1215

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Ser Asn Lys Ser Thr Ala Pro Asp Asp Leu Trp Val Leu Leu Ala Gln
 365 370 375
 ccc aac caa cag gac tga ctgactggca ggacaaggc tggcatggca 1263
 Pro Asn Gln Gln Asp
 380
 cagcaccact gccaggcctc cccaggcaca ccactctgcc caggaaatgg gggctttggg 1323
 tcatctccca ctgcctgggg gagtcagatg gggtgccagga atctggctct tcagccatct 1383
 caggtttagg gggtttgtaa cagacattat tctgtttca ctgcgtatcc ttggtaagcc 1443
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 ctctcgggcc atgctacccg gtatgactgg gtaatgagga cagactgtgg acaccccatc 1563
 tacctgagtc tgattctta gcagcagaga ctgaggggtg cagagtgtga gctggaaag 1623
 gtttgtggct cttgcagcc tccagggact ggcctgtccc caatagaatt gaagcagtcc 1683
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 <211> 382
 <212> PRT
 <213> Homo sapiens

 <400> 13

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 20 25 30

 Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
 35 40 45

 Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
 50 55 60

 Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
 65 70 75 80

 Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
 85 90 95

 Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
 100 105 110

 Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
 115 120 125

- 30 -

Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
130 135 140

Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
145 150 155 160

Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
165 170 175

Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
180 185 190

Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
195 200 205

Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
210 215 220

His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
225 230 235 240

Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
245 250 255

Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
260 265 270

Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
275 280 285

Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg
290 295 300

Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
305 310 315 320

Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
325 330 335

Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
340 345 350

Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
355 360 365

Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp

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370

375

380

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<211> 993
<212> DNA
<213> *Homo sapiens*

<220>
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<222> (1) .. (993)

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 Met Leu Pro Asp Trp Lys Ser Ser Leu Ile Leu Met Ala Tyr Ile Ile
 1 5 10 15
 atc ttc ctc act ggc ctc cct gcc aac ctc ctg gcc ctg cgg gcc ttt
 Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
 20 25 30
 gtg ggg cgg atc cgc cag ccc cag cct gca cct gtg cac atc ctc ctg
 Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
 35 40 45
 ctg agc ctg acg ctg gcc gac ctc ctc ctg ctg ctg ctg ccc ttc
 Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Pro Phe
 50 55 60
 aag atc atc gag gct gcg tcg aac ttc cgc tgg tac ctg ccc aag gtc
 Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
 65 70 75 80
 gtc tgc gcc ctc acg agt ttt ggc ttc tac agc agc atc tac tgc agc
 Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser
 85 90 95
 acg tgg ctc ctg gcg ggc atc agc atc gag cgc tac ctg gga gtg gct
 Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala
 100 105 110
 ttc ccc gtg cag tac aag ctc tcc cgc cgg cct ctg tat gga gtg att
 Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile
 115 120 125
 gca gct ctg gtg gcc tgg gtt atg tcc ttt ggt cac tgc acc atc gtg
 Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val
 130 135 140
 atc atc gtt caa tac ttg aac acg act gag cag gtc aga agt ggc aat
 Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn
 145 150 155 160
 gaa att acc tgc tac gag aac ttc acc gat aac cag ttg gac gtg gtg
 Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val
 165 170 175
 ctg ccc gtg cgg ctg gag ctg tgc ctg gtg ctc ttc ttc atc ccc atg
 Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met
 180 185 190

- 32 -

gca gtc acc atc ttc tgc tac tgg cgt ttt gtg tgg atc atg ctc tcc	624
Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser	
195 200 205	
cag ccc ctt gtg ggg gcc cag agg cgg cgc cga gcc gtg ggg ctg gct	672
Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Ala Val Gly Leu Ala	
210 215 220	
gtg gtg acg ctg ctc aat ttc ctg gtg tgc ttc gga cct tac aac gtg	720
Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val	
225 230 235 240	
tcc cac ctg gtg ggg tat cac cag aga aaa agc ccc tgg tgg cgg tca	768
Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser	
245 250 255	
ata gcc gtg gtg ttc agt tca ctc aac gcc agt ctg gac ccc ctg ctc	816
Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu	
260 265 270	
ttc tat ttc tct tca gtg gtg cgc agg gca ttt ggg aga ggg ctg	864
Phe Tyr Phe Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu	
275 280 285	
cag gtg ctg cgg aat cag ggc tcc tcc ctg ttg gga cgc aga ggc aaa	912
Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys	
290 295 300	
gac aca gca gag ggg aca aat gag gac agg ggt gtg ggt caa gga gaa	960
Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu	
305 310 315 320	
ggg atg cca agt tcg gac ttc act aca gag tag	993
Gly Met Pro Ser Ser Asp Phe Thr Thr Glu	
325 330	

<210> 15
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 15

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Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
 20 25 30

Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
 35 40 45

Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Pro Phe
 50 55 60

Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
 65 70 75 80

- 33 -

Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser
85 90 95

Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala
100 105 110

Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile
115 120 125

Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val
130 135 140

Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn
145 150 155 160

Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val
165 170 175

Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met
180 185 190

Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser
195 200 205

Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Ala Val Gly Leu Ala
210 215 220

Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val
225 230 235 240

Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser
245 250 255

Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu
260 265 270

Phe Tyr Phe Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu
275 280 285

Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys
290 295 300

Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu
305 310 315 320

- 34 -

Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
 325 330

<210> 16
 <211> 1287
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (72) .. (1085)

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 caggagcctg a atg ggg aac gat tct gtc agc tac gag tat ggg gat tac 110
 Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr
 1 5 10
 agc gac ctc tcg gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg 158
 Ser Asp Leu Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu
 15 20 25
 gcc atc gac ccg ctg cgc gtg gcc ccg ctc cca ctg tat gcc gcc atc 206
 Ala Ile Asp Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile
 30 35 40 45
 ttc ctg gtg ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg 254
 Phe Leu Val Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly
 50 55 60
 aag gtg gcc cgc ccg agg gtg ggt gcc acc tgg ttg ctc cac ctg gcc 302
 Lys Val Ala Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala
 65 70 75
 gtg gcg gat ttg ctg tgc tgt ttg tct ctg ccc atc ctg gca gtg ccc 350
 Val Ala Asp Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro
 80 85 90
 att gcc cgt gga ggc cac tgg ccg tat ggt gca gtg ggc tgt cgg gcg 398
 Ile Ala Arg Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala
 95 100 105
 ctg ccc tcc atc atc ctg ctg acc atg tat gcc agc gtc ctg ctc ctg 446
 Leu Pro Ser Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu
 110 115 120 125
 gca gct ctc agt gcc gac ctc tgc ttc ctg gct ctc ggg cct gcc tgg 494
 Ala Ala Leu Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp
 130 135 140
 tgg tct acg gtt cag cgg gcg tgc ggg gtg cag gtg gcc tgt ggg gca 542
 Trp Ser Thr Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala
 145 150 155
 gcc tgg aca ctg gcc ttg ctg ctc acc gtg ccc tcc gcc atc tac cgc 590
 Ala Trp Thr Leu Ala Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg
 160 165 170
 cgg ctg cac cag gag cac ttc cca gcc cgg ctg cag tgt gtg gac 638

- 35 -

Arg	Leu	His	Gln	Glu	His	Phe	Pro	Ala	Arg	Leu	Gln	Cys	Val	Val	Asp	
175					180					185						
tac ggc ggc tcc tcc agc acc gag aat gcg gtg act gcc atc cgg ttt															686	
Tyr	Gly	Gly	Ser	Ser	Ser	Thr	Glu	Asn	Ala	Val	Thr	Ala	Ile	Arg	Phe	
190					195					200					205	
ctt ttt ggc ttc ctg ggg ccc ctg gtg gcc gtg gcc agc tgc cac agt															734	
Leu	Phe	Gly	Phe	Leu	Gly	Pro	Leu	Val	Ala	Val	Ala	Ser	Cys	His	Ser	
															220	
210										215						
gcc ctc ctg tgc tgg gca gcc cga cgc tgc cgg ccg ctg ggc aca gcc															782	
Ala	Leu	Leu	Cys	Trp	Ala	Ala	Arg	Arg	Cys	Arg	Pro	Leu	Gly	Thr	Ala	
															235	
225										230						
att gtg gtg ggg ttt ttt gtc tgc tgg gca ccc tac cac ctg ctg ggg															830	
Ile	Val	Val	Gly	Phe	Phe	Val	Cys	Trp	Ala	Pro	Tyr	His	Leu	Leu	Gly	
															250	
240										245						
ctg gtg ctc act gtg gcg gcc ccg aac tcc gca ctc ctg gcc agg gcc															878	
Leu	Val	Leu	Thr	Val	Ala	Ala	Pro	Asn	Ser	Ala	Leu	Leu	Ala	Arg	Ala	
															265	
255										260						
ctg cgg gct gaa ccc ctc atc gtg ggc ctt gcc ctc gct cac agc tgc															926	
Leu	Arg	Ala	Glu	Pro	Leu	Ile	Val	Gly	Leu	Ala	Leu	Ala	His	Ser	Cys	
															285	
270										275						
ctc aat ccc atg ctc ttc ctg tat ttt ggg agg gct caa ctc cgc cgg															974	
Leu	Asn	Pro	Met	Leu	Phe	Leu	Tyr	Phe	Gly	Arg	Ala	Gln	Leu	Arg	Arg	
															300	
290										295						
tca ctg cca gct gcc tgt cac tgg gcc ctg agg gag tcc cag ggc cag															1022	
Ser	Leu	Pro	Ala	Ala	Cys	His	Trp	Ala	Leu	Arg	Glu	Ser	Gln	Gly	Gln	
															315	
305										310						
gac gaa agt gtg gac agc aag aaa tcc acc agc cat gac ctg gtc tcg															1070	
Asp	Glu	Ser	Val	Asp	Ser	Lys	Lys	Ser	Thr	Ser	His	Asp	Leu	Val	Ser	
															330	
320										325						
gag atg gag gtg tag gctggagaga cattgtgggt gtgtatcttc ttatctcatt															1125	
Glu	Met	Glu	Val													
335																
tcacaagact ggcttcaggc atagctggat ccaggagctc aatgatgtct tcattttatt															1185	
ccttccttca ttcaacagat atccatcatg cacttgctat gtgcaaggcc ttttttaggca															1245	
ctagagatat agcagtgacc aaaacagaca caaatcctgc cc															1287	

<210> 17
<211> 337
<212> PRT
<213> Homo sapiens

<400> 17

Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr Ser Asp Leu
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Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp

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20

25

30

Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
35 40 45

Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
50 55 60

Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
65 70 75 80

Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
85 90 95

Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
100 105 110

Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu Ala Ala Leu
115 120 125

Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr
130 135 140

Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr
145 150 155 160

Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His
165 170 175

Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly
180 185 190

Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly
195 200 205

Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu
210 215 220

Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val
225 230 235 240

Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu
245 250 255

Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala
260 265 270

Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
 275 280 285

Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
 290 295 300

Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
 305 310 315 320

Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu
 325 330 335

Val

<210> 18
 <211> 2858
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (174) .. (1175)

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 tgtttcttt tgtttgtata tatgtttatt ggtaacaggt gacactggaa gca atg 120
 Met
 1
 aac acc aca gtg atg caa ggc ttc aac aga tct gag cgg tgc ccc aga 224
 Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro Arg
 5 10 15
 gac act cgg ata gta cag ctg gta ttc cca gcc ctc tac aca gtg gtt 272
 Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val Val
 20 25 30
 ttc ttg acc ggc atc ctg ctg aat act ttg gct ctg tgg gtg ttt gtt 320
 Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe Val
 35 40 45
 cac atc ccc agc tcc tcc acc ttc atc atc tac ctc aaa aac act ttg 368
 His Ile Pro Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr Leu
 50 55 60 65
 gtg gcc gac ttg ata atg aca ctc atg ctt cct ttc aaa atc ctc tct 416
 Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu Ser
 70 75 80
 gac tca cac ctg gca ccc tgg cag ctc aga gct ttt gtg tgt cgt ttt 464
 Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg Phe

85	90	95	
tct tcg gtg ata ttt tat gag acc atg tat gtg ggc atc gtg ctg tta Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu Leu 100	105	110	512
ggg ctc ata gcc ttt gac aga ttc ctc aag atc atc aga cct ttg aga Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu Arg 115	120	125	560
aat att ttt cta aaa aaa cct gtt ttt gca aaa acg gtc tca atc ttc Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile Phe 130	135	140	608
atc tgg ttc ttt ttg ttc atc tcc ctg cca aat acg atc ttg agc Ile Trp Phe Phe Leu Phe Ile Ser Leu Pro Asn Thr Ile Leu Ser 150	155	160	656
aac aag gaa gca aca cca tcg tct gtg aaa aag tgt gct tcc tta aag Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu Lys 165	170	175	704
ggg cct ctg ggg ctg aaa tgg cat caa atg gta aat aac ata tgc cag Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys Gln 180	185	190	752
ttt att ttc tgg act gtt ttt atc cta atg ctt gtg ttt tat gtg gtt Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val Val 195	200	205	800
att gca aaa aaa gta tat gat tct tat aga aag tcc aaa agt aag gac Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys Asp 210	215	220	848
aga aaa aac aac aaa aag ctg gaa ggc aaa gta ttt gtt gtc gtg gct Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val Ala 230	235	240	896
gtc ttc ttt gtg tgt ttt gct cca ttt cat ttt gcc aga gtt cca tat Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro Tyr 245	250	255	944
act cac agt caa acc aac aat aag act gac tgt aga ctg caa aat caa Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn Gln 260	265	270	992
ctg ttt att gct aaa gaa aca act ctc ttt ttg gca gca act aac att Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn Ile 275	280	285	1040
tgt atg gat ccc tta ata tac ata ttc tta tgt aaa aaa ttc aca gaa Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr Glu 290	295	300	1088
aag cta cca tgt atg caa ggg aga aag acc aca gca tca agc caa gaa Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln Glu 310	315	320	1136
aat cat agc agt cag aca gac aac ata acc tta ggc tga caactgtaca Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly 325	330		1185

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tagggtaac ttctatttat tcatgagact tccgtagata atgtggaaat caaatttaac	1245
caagaaaaaa agatttggAAC aaatgctctc ttacattttt ttatcctcggt tacagaaaa	1305
gattatataa aattttaaatc cacatagatc tattcataag ctgaatgaac cattactaag	1365
agaatgcaac aggatacaaa tggccactag aggtcattat ttctttctt ctttttttt	1425
tttttaatt tcaagagcat ttcaactttaa cattttggaa aagactaagg agaaacgtat	1485
atccctacaa acctcccctc caaacacaccc ttccacattct ttccacaat tcacataaca	1545
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tcttgaagtc cattgctgaa aactgcagcc aggggttgaa agggatgcag acttgaagag	1665
tctgaggaac tgaagtgggt cagcaagacc tctgaaatcc tggtaaagg attttctcct	1725
tacaattaca aacagcctct ttccacattac aataatatac cataggaggc acaagcacca	1785
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taactattct ttgaaattct cttctgtcc agcaaatact ctaatgatgg ttaaacatgg	1905
cacctactca gcaatgcctt cctggaccac aaccctatc cccctgcccc accctccctca	1965
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agacatgcca gattttcttg gtatctccca taatacgacc tacagtccat ggtctacaga	2145
tgttttaat agaattgcta ttctcgatac atacaaagac gtaattgctg acccacaatc	2205
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ttggattttt ttcttgcatc cttctgtgat tcaaaaaagt aaaatgtggc tttctgaaat	2325
gatggataag agtctacatc ttcttagaaaa aatacataaa ggagtagttt agctctgtaa	2385
atgtgccacg agctccaaca cgaccatcggt agggtaagc ccacgttttc ttccatggcc	2445
tcaaaaggccc tagaacttgc ctacctttct ggccttaccc cctagctact tatccatctc	2505
ttgaacttta tactcttgc taaatttcta actttcagaa aatgccatac tctgtttgg	2565
caccacacat gtatatttcc ccctggtaca cttggaaagac tcttatccat ctgtgaaacc	2625
ctatgttgc atcacttgggt ccatgaaata ttacctggcc aatatcccac catcacctca	2685
aacccaatca cccctccctc tgtatgctgt cacacctata ttattaaact tatcacattg	2745
cattgttaatt acttcctgac ctttgcattct actcttttag taactgatgt atatatctga	2805
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<210> 19
 <211> 333
 <212> PRT
 <213> Homo sapiens

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<400> 19

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Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
20 25 30

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
35 40 45

Val His Ile Pro Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
50 55 60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
65 70 75 80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
85 90 95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
130 135 140

Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu
145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
225 230 235 240

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Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
325 330

<210> 20
<211> 878
<212> DNA
<213> Homo sapiens

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atctcttaaa tatgtggcaa actatggtc caaagagatg tggtccaaac ccgtcgaagg 180
ctttataattt tggtatttta taacaaggatg aacaaaactg acaataaaata ctccaaacgaa 240
ttatttttta aaataactaag gggcaaaggc tattcttaagg ggcaaaacaa tctattactc 300
agacctaccc gaaaatttca cgtgaagtcg atcaaaagtt atacaaaattt ggtatttaca 360
tgtttaaaat ccggattggc atttttctt aataataata catacaaaaa ctcagagggt 420
taataaaagaa ataattcaaa gtcctaataa gtcaacaaac agatttcatt ataagctgga 480
acataaaaga gacaccatgg ttggctgtct ctttcaaaa attatcacgg ccacttggc 540
aaacgggaag cagcatttcag aacaatggtt ctcaaatctc ggggtggcat aaacaccatg 600
caggttgggtt accacacaga ttccctggcc tggtccactt ctgaagctct cataaaggat 660
ctgaggaatc tgcttcgtga caagatttcag actatttattt tatttatacac ccaagctgga 720
gtgcagggtt gcaacccggt cagggaaacct cgcctcggag taaaaggaa accaaatcgg 780
ggcccaaggcc ctgagaatgg gttcaaacgg gcccaccacc ggttaacggta tcagaaaaaa 840
acggtccaga aggccagggg tcaaccgaac caagaagc 878

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<211> 1646
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (99) .. (743)

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	tgccaaagcc tgaaggctcc aagccataaa caacccca atg gcc tcc cac gaa gtt	116
	Met Ala Ser His Glu Val	
	1 5	
	gat aat gca gag ctg ggg tca gcc tct gcc cat ggt acc cca ggc agt	164
	Asp Asn Ala Glu Leu Gly Ser Ala Ser Ala His Gly Thr Pro Gly Ser	
	10 15 20	
	gag acg gga cca gaa gag ctg aat act tct gtc tac cac ccc ata aat	212
	Glu Thr Gly Pro Glu Glu Leu Asn Thr Ser Val Tyr His Pro Ile Asn	
	25 30 35	
	gga tca cca gat tat cag aaa gca aaa tta caa gtt ctt ggg gcc atc	260
	Gly Ser Pro Asp Tyr Gln Lys Ala Lys Leu Gln Val Leu Gly Ala Ile	
	40 45 50	
	cag atc ctg aat gca gca atg att ctg gct ttg ggt gtc ttt ctg ggt	308
	Gln Ile Leu Asn Ala Ala Met Ile Leu Ala Leu Gly Val Phe Leu Gly	
	55 60 65 70	
	tcc ttg caa tac cca tac cac ttc caa aag cac ttc ttt ttc ttc acc	356
	Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys His Phe Phe Phe Thr	
	75 80 85	
	ttc tac aca ggc tac ccg att tgg ggt gct gtg ttt ttc tgt agt tca	404
	Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala Val Phe Phe Cys Ser Ser	
	90 95 100	
	gga acc ttg tct gta gca ggg ata aaa ccc aca aga aca tgg ata	452
	Gly Thr Leu Ser Val Val Ala Gly Ile Lys Pro Thr Arg Thr Trp Ile	
	105 110 115	
	cag aac agt ttt gga atg aac att gcc agt gct aca att gca cta gtg	500
	Gln Asn Ser Phe Gly Met Asn Ile Ala Ser Ala Thr Ile Ala Leu Val	
	120 125 130	
	ggg act gct ttt ctc tca cta aat ata gca gtt aat atc cag tca tta	548
	Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala Val Asn Ile Gln Ser Leu	
	135 140 145 150	
	agg agt tgt cac tct tca tca gag tca ccg gac cta tgc aat tac atg	596
	Arg Ser Cys His Ser Ser Ser Glu Ser Pro Asp Leu Cys Asn Tyr Met	
	155 160 165	
	ggc tcc ata tca aat ggc atg gtg tct cta ctg ctg att ctc acc ttg	644
	Gly Ser Ile Ser Asn Gly Met Val Ser Leu Leu Leu Ile Leu Thr Leu	
	170 175 180	
	ctg gaa tta tgc gta act atc tct acc ata gcc atg tgg tgc aat gca	692
	Leu Glu Leu Cys Val Thr Ile Ser Thr Ile Ala Met Trp Cys Asn Ala	

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	185	190	195	
aac tgc tgt aat tca aga gag gaa att tcc tca cct ccc aat tct gtg Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser Ser Pro Pro Asn Ser Val	200	205	210	740
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ttaaatctcc agtgactcag agcttcaccc acaaactcag gagaacataa gcctgctcgt				853
aaagctcaat cttcttatca tggcaccaat cacaagaacc ttggacgttt gactgactct				913
atcctttctc tcctaactat aaatcctatt tgtgtgtcgt gggtatggaa ggacagatat				973
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cagaaattgg ttctatattct tcttatccac ctactccatt gctttatgag gtttaaggaa				1093
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gttaggaagaa aaatgagaca tttttccat tacagagaaa tgcttcttga cttaacatc				1213
agcattataa aaagtgtcaa ataaaaaatt accatcatta tcattaaaat aaattttcac				1273
tgtatttgag atgggagggt taaggctcag ggattttatt tcagtgaact gctggaactc				1333
acacatgccc tgatatgtaa atgatgattt atgttggcga gtctgagagc aagccaaat				1393
gtgttcttca aaggacaatg ggaaactgta aagtagagaa ctaaagaata aggcctttag				1453
aatctgacac atctgggttc aaattctgaa actgtcactt attacctgta tgaacatggg				1513
caaattatct aatctctctg atctatttt cctcatctgt aaaataggtg taataataac				1573
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ccacaggtac ttg				1646

<210> 22
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Ala Ser His Glu Val Asp Asn Ala Glu Leu Gly Ser Ala Ser Ala	1	5	10	15
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His Gly Thr Pro Gly Ser Glu Thr Gly Pro Glu Glu Leu Asn Thr Ser	20	25	30
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Val Tyr His Pro Ile Asn Gly Ser Pro Asp Tyr Gln Lys Ala Lys Leu	35	40	45
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Gln Val Leu Gly Ala Ile Gln Ile Leu Asn Ala Ala Met Ile Leu Ala	50	55	60
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Leu Gly Val Phe Leu Gly Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys
65 70 75 80

His Phe Phe Phe Phe Thr Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala
85 90 95

Val Phe Phe Cys Ser Ser Gly Thr Leu Ser Val Val Ala Gly Ile Lys
100 105 110

Pro Thr Arg Thr Trp Ile Gln Asn Ser Phe Gly Met Asn Ile Ala Ser
115 120 125

Ala Thr Ile Ala Leu Val Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala
130 135 140

Val Asn Ile Gln Ser Leu Arg Ser Cys His Ser Ser Ser Glu Ser Pro
145 150 155 160

Asp Leu Cys Asn Tyr Met Gly Ser Ile Ser Asn Gly Met Val Ser Leu
165 170 175

Leu Leu Ile Leu Thr Leu Leu Glu Leu Cys Val Thr Ile Ser Thr Ile
180 185 190

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gcacggcaga gagtctggtg gggtgagggg gctggcctgg cccctctgtc ctgtggaa 178
atg ctg ggg caa gtg gtc acc ctc ata ctc ctc ctg ctc aag gtg 226
Met Leu Gly Gln Val Val Thr Leu Ile Leu Leu Leu Lys Val
1 5 10 15

tat cag ggc aaa gga tgc cag gga tca gct gac cat gtg gtt agc atc 274

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Tyr	Gln	Gly	Lys	Gly	Cys	Gln	Gly	Ser	Ala	Asp	His	Val	Val	Ser	Ile	
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tcg gga gtg cct ctt cag tta caa cca aac agc ata cag acg aag gtt															322	
Ser	Gly	Val	Pro	Leu	Gln	Leu	Gln	Pro	Asn	Ser	Ile	Gln	Thr	Lys	Val	
35						40						45				
gac agc att gca tgg aag aag ttg ctg ccc tca caa aat gga ttt cat															370	
Asp	Ser	Ile	Ala	Trp	Lys	Lys	Leu	Leu	Pro	Ser	Gln	Asn	Gly	Phe	His	
50						55						60				
cac ata ttg aag tgg gag aat ggc tct ttg cct tcc aat act tcc aat															418	
His	Ile	Leu	Lys	Trp	Glu	Asn	Gly	Ser	Leu	Pro	Ser	Asn	Thr	Ser	Asn	
65						70						75			80	
gat aga ttc agt ttt ata gtc aag aac ttg agt ctt ctc atc aag gca															466	
Asp	Arg	Phe	Ser	Phe	Ile	Val	Lys	Asn	Leu	Ser	Leu	Ile	Lys	Ala		
85						90						95				
gct cag cag cag gac agt ggc ctc tac tgc ctg gag gtc acc agt ata															514	
Ala	Gln	Gln	Gln	Asp	Ser	Gly	Leu	Tyr	Cys	Leu	Glu	Val	Thr	Ser	Ile	
100						105						110				
tct gga aaa gtt cag aca gcc acg ttc cag gtt ttt gta ttt gat aaa															562	
Ser	Gly	Lys	Val	Gln	Thr	Ala	Thr	Phe	Gln	Val	Phe	Val	Phe	Asp	Lys	
115						120						125				
gtt gag aaa ccc cgc cta cag ggg cag ggg aag atc ctg gac aga ggg															610	
Val	Glu	Lys	Pro	Arg	Leu	Gln	Gly	Gln	Gly	Lys	Ile	Leu	Asp	Arg	Gly	
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aga tgc caa gtg gct ctg tct tgc ttg gtc tcc agg gat ggc aat gtg															658	
Arg	Cys	Gln	Val	Ala	Leu	Ser	Cys	Leu	Val	Ser	Arg	Asp	Gly	Asn	Val	
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tcc tat gct tgg tac aga ggg agc aag ctg atc cag aca gca ggg aac															706	
Ser	Tyr	Ala	Trp	Tyr	Arg	Gly	Ser	Lys	Leu	Ile	Gln	Thr	Ala	Gly	Asn	
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ctc acc tac ctg gac gag gag gtt gac att aat ggc act cac aca tat															754	
Leu	Thr	Tyr	Leu	Asp	Glu	Glu	Val	Asp	Ile	Asn	Gly	Thr	His	Thr	Tyr	
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acc tgc aat gtc agc aat cct gtt agc tgg gaa agc cac acc ctg aat															802	
Thr	Cys	Asn	Val	Ser	Asn	Pro	Val	Ser	Trp	Glu	Ser	His	Thr	Leu	Asn	
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ctc act cag gac tgt cag aat gcc cat cag gaa ttc aga ttt tgg ccg															850	
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Phe	Leu	Val	Ile	Ile	Val	Ile	Leu	Ser	Ala	Leu	Phe	Leu	Gly	Thr	Leu	
225						230						235			240	
gcc tgc ttc tgt gtg tgg agg aga aag agg aag gag aag cag tca gag															946	
Ala	Cys	Phe	Cys	Val	Trp	Arg	Arg	Lys	Arg	Lys	Glu	Lys	Gln	Ser	Glu	
245						250						255				
acc agt ccc aag gaa ttt ttg aca att tac gaa gat gtc aag gat ctg															994	
Thr	Ser	Pro	Lys	Glu	Phe	Leu	Thr	Ile	Tyr	Glu	Asp	Val	Lys	Asp	Leu	
260						265						270				

aaa acc agg aga aat cac gag cag gag cag act ttt cct gga ggg ggg	1042
Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly	
275 280 285	
agc acc atc tac tct atg atc cag tcc cag tct tct gct ccc acg tca	1090
Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser	
290 295 300	
caa gaa cct gca tat aca tta tat tca tta att cag cct tcc agg aag	1138
Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys	
305 310 315 320	
tct gga tcc agg aag agg aac cac agc cct tcc ttc aat agc act atc	1186
Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile	
325 330 335	
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Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg	
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Leu Ser Arg Lys Glu Leu Glu Asn Phe Asp Val Tyr Ser	
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 35 40 45

Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
 50 55 60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
 65 70 75 80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
 85 90 95

Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
 100 105 110

Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys
 115 120 125

Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly
 130 135 140

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val
 145 150 155 160

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn
 165 170 175

Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr
 180 185 190

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn

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195

200

205

Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro
 210 215 220

Phe Leu Val Ile Ile Val Ile Leu Ser Ala Leu Phe Leu Gly Thr Leu
 225 230 235 240

Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu
 245 250 255

Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu
 260 265 270

Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly
 275 280 285

Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser
 290 295 300

Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys
 305 310 315 320

Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile
 325 330 335

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ggggggcccccgg aggccgcagc ttgcctgcgc gctctgagcc ttgcgaactc gcgagcaaag 180

tttgggtggag gcaacgccaa gcctgagtcc tttcttcctc tcgttcccca aatccgaggc 240

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ataacgtcc	acatggagat	atgaaagagg	accggggatt	gttaccgtaa	cc atg gtc	598
					Met Val	
					1	
agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc acc atg gca acc ttg						646
Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala Thr Leu						
5	10	15				
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Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu						
20	25	30				
cca gaa gag cca cca acc aaa tac caa atc tct caa cca gaa gtg tac						742
Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr						
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gtg gct gcg cca ggg gag tcg cta gag gtg cgc tgc ctg ttg aaa gat						790
Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp						
55	60	65				
gcc gcc gtg atc agt tgg act aag gat ggg gtg cac ttg ggg ccc aac						838
Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn						
70	75	80				
aat agg aca gtg ctt att ggg gag tac ttg cag ata aag ggc gcc acg						886
Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr						
85	90	95				
cct aga gac tcc ggc ctc tat gct tgt act gcc agt agg act gta gac						934
Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp						
100	105	110				
agt gaa act tgg tac ttc atg gtg aat gtc aca gat gcc atc tca tcc						982
Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser						
115	120	125	130			
gga gat gat gag gat gac acc gat ggt gcg gaa gat ttt gtc agt gag						1030
Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu						
135	140	145				
aac agt aac aac aag aga gca cca tac tgg acc aac aca gaa aag atg						1078
Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met						
150	155	160				
gaa aag cgg ctc cat gct gtg cct gcg gcc aac act gtc aag ttt cgc						1126
Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg						
165	170	175				
tgc cca gcc ggg ggg aac cca atg cca acc atg cgg tgg ctg aaa aac						1174
Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn						
180	185	190				

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Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg	
195 200 205 210	
aac cag cac tgg agc ctc att atg gaa agt gtg gtc cca tct gac aag	1270
Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys	
215 220 225	
gga aat tat acc tgt gtg gag aat gaa tac ggg tcc atc aat cac	1318
Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His	
230 235 240	
acg tac cac ctg gat gtt gtg gag cga tcg cct cac cgg ccc atc ctc	1366
Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu	
245 250 255	
caa gcc gga ctg ccg gca aat gcc tcc aca gtg gtc gga gga gac gta	1414
Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val	
260 265 270	
gag ttt gtc tgc aag gtt tac agt gat gcc cag ccc cac atc cag tgg	1462
Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp	
275 280 285 290	
atc aag cac gtg gaa aag aac ggc agt aaa tac ggg ccc gac ggg ctg	1510
Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu	
295 300 305	
ccc tac ctc aag gtt ctc aag cac tcg ggg ata aat agt tcc aat gca	1558
Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser Asn Ala	
310 315 320	
gaa gtg ctg gct ctg ttc aat gtg acc gag gcg gat gct ggg gaa tat	1606
Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly Glu Tyr	
325 330 335	
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Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser Ala Trp	
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Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val	
375 380 385	
tcc tta atc gcc tgt atg gtg gta aca gtc atc ctg tgc cga atg aag	1798
Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys	
390 395 400	
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Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys	
405 410 415	
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Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu	
420 425 430	
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Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr	

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cgc ctc tct tca acg gca gac acc ccc atg ctg gca ggg gtc tcc gag				1990
Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu				
455	460	465		
tat gaa ctt cca gag gac cca aaa tgg gag ttt cca aga gat aag ctg				2038
Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu				
470	475	480		
aca ctg ggc aag ccc ctg gga gaa ggt tgc ttt ggg caa gtg gtc atg				2086
Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met				
485	490	495		
gcg gaa gca gtg gga att gac aaa gac aag ccc aag gag gcg gtc acc				2134
Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr				
500	505	510		
gtg gcc gtg aag atg ttg aaa gat gat gcc aca gag aaa gac ctt tct				2182
Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser				
515	520	525	530	
gat ctg gtg tca gag atg gag atg atg aag atg att ggg aaa cac aag				2230
Asp Leu Val Ser Glu Met Glu Met Lys Met Ile Gly Lys His Lys				
535	540	545		
aat atc ata aat ctt ctt gga gcc tgc aca cag gat ggg cct ctc tat				2278
Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr				
550	555	560		
gtc ata gtt gag tat gcc tct aaa ggc aac ctc cga gaa tac ctc cga				2326
Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg				
565	570	575		
gcc cgg agg cca ccc ggg atg gag tac tcc tat gac att aac cgt gtt				2374
Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val				
580	585	590		
cct gag gag cag atg acc ttc aag gac ttg gtg tca tgc acc tac cag				2422
Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln				
595	600	605	610	
ctg gcc aga ggc atg gag tac ttg gct tcc caa aaa tgt att cat cga				2470
Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg				
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Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys				
630	635	640		
ata gca gac ttt gga ctc gcc aga gat atc aac aat ata gac tat tac				2566
Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr				
645	650	655		
aaa aag acc acc aat ggg cgg ctt cca gtc aag tgg atg gct cca gaa				2614
Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu				
660	665	670		
gcc ctg ttt gat aga gta tac act cat cag agt gat gtc tgg tcc ttc				2662
Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe				
675	680	685	690	

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Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg	
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atg gat aag cca gcc aac tgc acc aac gaa ctg tac atg atg atg agg	2806
Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg	
725 730 735	
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Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu	
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Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Asn Glu Glu Tyr	
755 760 765 770	
ttg gac ctc agc caa cct ctc gaa cag tat tca cct agt tac cct gac	2950
Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp	
775 780 785	
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Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp	
790 795 800	
ccc atg cct tac gaa cca tgc ctt cct cag tat cca cac ata aac ggc	3046
Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly	
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<210> 26
 <211> 822
 <212> PRT
 <213> Homo sapiens

<400> 26

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10	15		

Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr			
20	25	30	
30			

Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu			
35	40	45	
45			

Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu			
50	55	60	
60			

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly			
65	70	75	80
75	80		

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly			
85	90	95	
95			

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr			
100	105	110	
110			

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile			
115	120	125	
125			

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Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
245 250 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
260 265 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
275 280 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305 310 315 320

Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
325 330 335

Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
340 345 350

Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
355 360 365

- 55 -

Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
370 375 380

Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385 390 395 400

Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
405 410 415

His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
420 425 430

Ala Glu Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
435 440 445

Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
450 455 460

Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465 470 475 480

Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
485 490 495

Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
500 505 510

Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
515 520 525

Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
530 535 540

His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545 550 555 560

Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
565 570 575

Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
580 585 590

Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
595 600 605

Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
610 615 620

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His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625 630 635 640

Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
645 650 655

Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
660 665 670

Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
675 680 685

Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
690 695 700

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705 710 715 720

His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
725 730 735

Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
740 745 750

Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
755 760 765

Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
770 775 780

Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
785 790 795 800

Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile
805 810 815

Asn Gly Ser Val Lys Thr
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<210> 27
<211> 5175
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

- 57 -

<222> (94)..(2676)

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gct	gtg	gcc	acc	tgt	cgc	cct	gac	gaa	tgc	cag	tgc	tct	gat	gga	aac	834
Ala	Val	Ala	Thr	Cys	Arg	Pro	Asp	Glu	Phe	Gln	Cys	Ser	Asp	Gly	Asn	
235								240					245			
tgc	atc	cat	ggc	agc	cg	cag	tgt	gac	cg	gaa	tat	gac	tgc	aag	gac	882
Cys	Ile	His	Gly	Ser	Arg	Gln	Cys	Asp	Arg	Glu	Tyr	Asp	Cys	Lys	Asp	
250								255				260				
atg	agc	gat	gaa	gtt	ggc	tgc	gtt	aat	gtg	aca	ctc	tgc	gag	gga	ccc	930
Met	Ser	Asp	Glu	Val	Gly	Cys	Val	Asn	Val	Thr	Leu	Cys	Glu	Gly	Pro	
265								270				275				
aac	aag	ttc	aag	tgt	cac	agc	ggc	gaa	tgc	atc	acc	ctg	gac	aaa	gtc	978
Asn	Lys	Phe	Lys	Cys	His	Ser	Gly	Glu	Cys	Ile	Thr	Leu	Asp	Lys	Val	
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tgc	aac	atg	gct	aga	gac	tgc	cg	gac	tgg	tca	gat	gaa	ccc	atc	aaa	1026
Cys	Asn	Met	Ala	Arg	Asp	Cys	Arg	Asp	Trp	Ser	Asp	Glu	Pro	Ile	Lys	
300								305					310			
gag	tgc	ggg	acc	aac	gaa	tgc	ttg	gac	aac	aa	ggc	ggc	tgt	tcc	cac	1074
Glu	Cys	Gly	Thr	Asn	Glu	Cys	Leu	Asp	Asn	Asn	Gly	Gly	Cys	Ser	His	
315								320					325			
gtc	tgc	aat	gac	ctt	aag	atc	ggc	tac	gag	tgc	ctg	tgc	ccc	gac	ggc	1122
Val	Cys	Asn	Asp	Leu	Lys	Ile	Gly	Tyr	Glu	Cys	Leu	Cys	Pro	Asp	Gly	
330								335					340			
tcc	cag	ctg	gtg	gcc	cag	cga	aga	tgc	gaa	gat	atc	gat	gag	tgt	cag	1170
Phe	Gln	Leu	Val	Ala	Gln	Arg	Arg	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Gln	
345								350				355				
gat	ccc	gac	acc	tgc	agc	cag	ctc	tgc	gtg	aac	ctg	gag	ggt	ggc	tac	1218
Asp	Pro	Asp	Thr	Cys	Ser	Gln	Leu	Cys	Val	Asn	Leu	Glu	Gly	Gly	Tyr	
360								365				370			375	
aag	tgc	cag	tgt	gag	gaa	ggc	ttc	cag	ctg	gac	ccc	cac	acg	aag	gcc	1266
Lys	Cys	Gln	Cys	Glu	Glu	Gly	Phe	Gln	Leu	Asp	Pro	His	Thr	Lys	Ala	
380								385					390			
tgc	aag	gct	gtg	ggc	tcc	atc	gcc	tac	ctc	ttc	acc	aa	ccg	cac		1314
Cys	Lys	Ala	Val	Gly	Ser	Ile	Ala	Tyr	Leu	Phe	Phe	Thr	Asn	Arg	His	
395								400				405				
gag	gtc	agg	aag	atg	acg	ctg	gac	cg	agc	gag	tac	acc	agc	ctc	atc	1362
Glu	Val	Arg	Lys	Met	Thr	Leu	Asp	Arg	Ser	Glu	Tyr	Thr	Ser	Leu	Ile	
410								415				420				
ccc	aac	ctg	agg	aac	gtg	gtc	gct	ctg	gac	acg	gag	gtg	gcc	agc	aat	1410
Pro	Asn	Leu	Arg	Asn	Val	Val	Ala	Leu	Asp	Thr	Glu	Val	Ala	Ser	Asn	
425								430				435				
aga	atc	tac	tgg	tct	gac	ctg	tcc	cag	aga	atg	atc	tgc	agc	acc	cag	1458
Arg	Ile	Tyr	Trp	Ser	Asp	Leu	Ser	Gln	Arg	Met	Ile	Cys	Ser	Thr	Gln	
440								445				450			455	
ctt	gac	aga	gcc	cac	ggc	gtc	tct	tcc	tat	gac	acc	gtc	atc	agc	agg	1506
Leu	Asp	Arg	Ala	His	Gly	Val	Ser	Ser	Tyr	Asp	Thr	Val	Ile	Ser	Arg	
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gac atc cag gcc ccc gac ggg ctg gct gtg gac tgg atc cac agc aac	1554
Asp Ile Gln Ala Pro Asp Gly Leu Ala Val Asp Trp Ile His Ser Asn	
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atc tac tgg acc gac tct gtc ctg ggc act gtc tct gtt gcg gat acc	1602
Ile Tyr Trp Thr Asp Ser Val Leu Gly Thr Val Ser Val Ala Asp Thr	
490 495 500	
aag ggc gtg aag agg aaa acg tta ttc agg gag aac ggc tcc aag cca	1650
Lys Gly Val Lys Arg Lys Thr Leu Phe Arg Glu Asn Gly Ser Lys Pro	
505 510 515	
agg gcc atc gtg gtg gat cct gtt cat ggc ttc atg tac tgg act gac	1698
Arg Ala Ile Val Val Asp Pro Val His Gly Phe Met Tyr Trp Thr Asp	
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tgg gga act ccc gcc aag atc aag aaa ggg ggc ctg aat ggt gtg gac	1746
Trp Gly Thr Pro Ala Lys Ile Lys Lys Gly Gly Leu Asn Gly Val Asp	
540 545 550	
atc tac tcg ctg gtg act gaa aac att cag tgg ccc aat ggc atc acc	1794
Ile Tyr Ser Leu Val Thr Glu Asn Ile Gln Trp Pro Asn Gly Ile Thr	
555 560 565	
cta gat ctc ctc agt ggc cgc ctc tac tgg gtt gac tcc aaa ctt cac	1842
Leu Asp Leu Leu Ser Gly Arg Leu Tyr Trp Val Asp Ser Lys Leu His	
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tcc atc tca agc atc gat gtc aat ggg ggc aac cgg aag acc atc ttg	1890
Ser Ile Ser Ser Ile Asp Val Asn Gly Gly Asn Arg Lys Thr Ile Leu	
585 590 595	
gag gat gaa aag agg ctg gcc cac ccc ttc tcc ttg gcc gtc ttt gag	1938
Glu Asp Glu Lys Arg Leu Ala His Pro Phe Ser Leu Ala Val Phe Glu	
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gac aaa gta ttt tgg aca gat atc atc aac gaa gcc att ttc agt gcc	1986
Asp Lys Val Phe Trp Thr Asp Ile Ile Asn Glu Ala Ile Phe Ser Ala	
620 625 630	
aac cgc ctc aca ggt tcc gat gtc aac ttg ttg gct gaa aac cta ctg	2034
Asn Arg Leu Thr Gly Ser Asp Val Asn Leu Leu Ala Glu Asn Leu Leu	
635 640 645	
tcc cca gag gat atg gtc ctc ttc cac aac ctc acc cag cca aga gga	2082
Ser Pro Glu Asp Met Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly	
650 655 660	
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Val Asn Trp Cys Glu Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr	
665 670 675	
ctg tgc ctc cct gcc ccg cag atc aac ccc cac tcg ccc aag ttt acc	2178
Leu Cys Leu Pro Ala Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr	
680 685 690 695	
tgc gcc tgc ccg gac ggc atg ctg ctg gcc agg gac atg agg agc tgc	2226
Cys Ala Cys Pro Asp Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys	
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ctc aca gag gct gag gct gca gtg gcc acc cag gag aca tcc acc gtc	2274

- 60 -

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tcttaaatg						5175

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<210> 28

<211> 860

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val Ala Leu Leu Leu
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20 25 30

Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly
35 40 45

Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu
50 55 60

Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn
65 70 75 80

Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp
85 90 95

Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp
100 105 110

Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
115 120 125

Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
130 135 140

Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys
145 150 155 160

Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly
165 170 175

Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly
180 185 190

Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu
195 200 205

Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp
210 215 220

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Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu
225 230 235 240

Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln Cys Asp
245 250 255

Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys Val Asn
260 265 270

Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu
275 280 285

Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp
290 295 300

Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp
305 310 315 320

Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr
325 330 335

Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys
340 345 350

Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys
355 360 365

Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly Phe Gln
370 375 380

Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile Ala Tyr
385 390 395 400

Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu Asp Arg
405 410 415

Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val Ala Leu
420 425 430

Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln
435 440 445

Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser
450 455 460

Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala

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465	470	475	480
val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly			
485	490	495	
Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe			
500	505	510	
Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His			
515	520	525	
Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys			
530	535	540	
Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile			
545	550	555	560
Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr			
565	570	575	
Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly			
580	585	590	
Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro			
595	600	605	
Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile			
610	615	620	
Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn			
625	630	635	640
Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His			
645	650	655	
Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu			
660	665	670	
Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn			
675	680	685	
Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu			
690	695	700	
Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala			
705	710	715	720

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Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val
725 730 735

Arg Thr Gln His Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
740 745 750

Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
755 760 765

His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
770 775 780

Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
785 790 795 800

Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
805 810 815

Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
820 825 830

Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser Tyr Pro
835 840 845

Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala
850 855 860

<210> 29

<211> 2070

<212> DNA

<213> Homo sapiens

<400> 29

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ccccccactc tccttaggg agctgagggtt cttctgcct gagccctgca gcagcggcag	1740
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ccctgaagtg gggacggaat agactcacat taggttttagt ttgtgaaaac tccatccago	1860
taagcgatct tgaacaagtc acaacctccc aggctcctca tttgctagtc acggacagtg	1920
attcctgcct cacaggtgaa gattaaagag acaacgaatg tgaatcatgc ttgcaggttt	1980
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 Met Thr Pro Ile Leu Thr Val Leu Ile
 1 5

tgt ctc ggg ctg agt ctg ggc ccc agg acc cac gtg cag gca ggg cac 162
 Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Val Gln Ala Gly His
 10 15 20 25

ctc ccc aag ccc acc ctc tgg gct gag cca ggc tct gtg atc atc cag 210
 Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile Ile Gln
 30 35 40

gga agt cct gtg acc ctc agg tgt cag ggg agc ctt cag gct gag gag 258
 Gly Ser Pro Val Thr Leu Arg Cys Gln Gly Ser Leu Gln Ala Glu Glu
 45 50 55

tac cat cta tat agg gaa aac aaa tca gca tcc tgg gtt aga cgg ata 306
 Tyr His Leu Tyr Arg Glu Asn Lys Ser Ala Ser Trp Val Arg Arg Ile
 60 65 70

caa gag cct ggg aag aat ggc cag ttc ccc atc cca tcc atc acc tgg 354
 Gln Glu Pro Gly Lys Asn Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp
 75 80 85

gaa cac gca ggg cgg tat cac tgt cag tac tac agc cac aat cac tca 402
 Glu His Ala Gly Arg Tyr His Cys Gln Tyr Tyr Ser His Asn His Ser
 90 95 100 105

tca gag tac agt gac ccc ctg gag ctg gtg gtg aca gga gcc tac agc 450
 Ser Glu Tyr Ser Asp Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ser
 110 115 120

aaa ccc acc ctc tca gct ctg ccc agc cct gtg gtg acc tta gga ggg 498
 Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Val Val Thr Leu Gly Gly
 125 130 135

aac gtg acc ctc cag tgt gtc tca cag gtg gca ttt gac ggc ttc att 546
 Asn Val Thr Leu Gln Cys Val Ser Gln Val Ala Phe Asp Gly Phe Ile
 140 145 150

ctg tgt aag gaa gga gaa gat gaa cac cca caa cgc ctg aac tcc cat 594
 Leu Cys Lys Glu Gly Glu Asp Glu His Pro Gln Arg Leu Asn Ser His
 155 160 165

tcc cat gcc cgt ggg tgg tcc tgg gcc atc ttc tcc gtg ggc ccc gtg 642
 Ser His Ala Arg Gly Trp Ser Trp Ala Ile Phe Ser Val Gly Pro Val
 170 175 180 185

agc ccg agt cgc agg tgg tcg tac agg tgc tat gct tat gac tcg aac 690
 Ser Pro Ser Arg Arg Trp Ser Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn
 190 195 200

tct ccc tat gtg tgg tct cta ccc agt gat ctc ctg gag ctc ctg gtc 738
 Ser Pro Tyr Val Trp Ser Leu Pro Ser Asp Leu Leu Glu Leu Leu Val
 205 210 215

cca ggt gtt tct aag aag cca tca ctc tca gtg cag cca ggt cct atg 786
 Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Met
 220 225 230

gtg gcc cct ggg gag agc ctg acc ctc cag tgt gtc tct gat gtc ggc	834
Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys Val Ser Asp Val Gly	
235 240 245	
tac gac aga ttt gtt ctg tat aag gag gga gaa cgt gac ttc ctc cag	882
Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu Arg Asp Phe Leu Gln	
250 255 260 265	
cgc cct ggt tgg cag ccc cag gct ggg ctc tcc cag gcc aac ttc acc	930
Arg Pro Gly Trp Gln Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr	
270 275 280	
ctg ggc cct gtg agc ccc tcc cac ggg ggc cag tac aga tgc tac agt	978
Leu Gly Pro Val Ser Pro Ser His Gly Gly Gln Tyr Arg Cys Tyr Ser	
285 290 295	
gca cac aac ctc tcc tcc gag tgg tcg gcc ccc agt gac ccc ctg gac	1026
Ala His Asn Leu Ser Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp	
300 305 310	
atc ctg atc aca gga cag ttc tat gac aga ccc tct ctc tcg gtg cag	1074
Ile Leu Ile Thr Gly Gln Phe Tyr Asp Arg Pro Ser Leu Ser Val Gln	
315 320 325	
ccg gtc ccc aca gta gcc cca gga aag aac gtg acc ctg ctg tgt cag	1122
Pro Val Pro Thr Val Ala Pro Gly Lys Asn Val Thr Leu Leu Cys Gln	
330 335 340 345	
tca cgg ggg cag ttc cac act ttc ctt ctg acc aag gag ggg gca ggc	1170
Ser Arg Gly Gln Phe His Thr Phe Leu Leu Thr Lys Glu Gly Ala Gly	
350 355 360	
cat ccc cca ctg cat ctg aga tca gag cac caa gct cag cag aac cag	1218
His Pro Pro Leu His Leu Arg Ser Glu His Gln Ala Gln Gln Asn Gln	
365 370 375	
gct gaa ttc cgc atg ggt cct gtg acc tca gcc cac gtg ggg acc tac	1266
Ala Glu Phe Arg Met Gly Pro Val Thr Ser Ala His Val Gly Thr Tyr	
380 385 390	
aga tgc tac agc tca ctc agc tcc aac ccc tac ctg ctg tct ctc ccc	1314
Arg Cys Tyr Ser Ser Leu Ser Ser Asn Pro Tyr Leu Leu Ser Leu Pro	
395 400 405	
agt gac ccc ctg gag ctc gtg gtc tca gca tcc cta ggc caa cac ccc	1362
Ser Asp Pro Leu Glu Leu Val Val Ser Ala Ser Leu Gly Gln His Pro	
410 415 420 425	
cag gat tac aca gtg gag aat ctc atc cgc atg ggt gtg gct ggc ttg	1410
Gln Asp Tyr Thr Val Glu Asn Leu Ile Arg Met Gly Val Ala Gly Leu	
430 435 440	
gtc ctg gtg gtc ctc ggg att ctg cta ttt gag gct cag cac agc cag	1458
Val Leu Val Val Leu Gly Ile Leu Leu Phe Glu Ala Gln His Ser Gln	
445 450 455	
aga agc cta caa gat gca gcc ggg agg tga acagcagaga ggacaatgca	1508
Arg Ser Leu Gln Asp Ala Ala Gly Arg	
460 465	
tacttcagcg tggggagcc tcagggacag atctgatgat cccaggaggc tctggaggac	1568

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aatctaggac ctacattatc tggactgtat gctggtcatt tctagagaca gcaatcaata 1628
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Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
 20 25 30

Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
 35 40 45

Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
 50 55 60

Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
 65 70 75 80

Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
 85 90 95

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
 100 105 110

Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
 115 120 125

Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
 130 135 140

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
 145 150 155 160

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
 165 170 175

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
 180 185 190

- 70 -

Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
195 200 205

Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro
210 215 220

Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
225 230 235 240

Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
245 250 255

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
260 265 270

Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser
275 280 285

His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
290 295 300

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
305 310 315 320

Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
325 330 335

Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
340 345 350

Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
355 360 365

Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
370 375 380

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
385 390 395 400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
405 410 415

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
420 425 430

Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile

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435

440

445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
450 455 460

Gly Arg
465